#6

SEQUENCE LISTING

<110> Wolosker, Herman
Takashashi, Maasaki
Mothet, Jean-Pierre
Ferris, Christopher
Snyder, Solomon

<120> Mammalian Serine Racemase

<130> 001107.00171

<160> 11

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<212> DNA
<213> Mus musculus

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cctgcttaca ttgtggttcc ccaaacagct cccaactgca agaaactggc aatccaagcc 360
tatggagcat cgatagtata ctgtgaccca agtgacgagt ccagagaaaa ggtcactcaa 420
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gctggacaag gaacaattgc cctggaagtg ctgaaccagg ttcccttggt agatgcactg 540
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ccattttgaa tcaactaaca gggcgcaatc ttttcttcaa atgtgaactc ttccagaaaa 180
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acatcccaac caggaacctg cagtgatagc tggacaaggg acaattgccc tggaagtgct 540
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<400> 5

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<211> 27
<212> PRT
<213> Rat rattus

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Gln His Phe Gln Thr Val Ser Pro Glu Val Lys
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<210> 7
<211> 25
<212> PRT
<213> Rat rattus

<400> 7

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1 5 10 15

Ser Ile Leu Asn Gln Ile Ala Gly Arg
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<210> 8
<211> 339
<212> PRT
<213> Mus musculus

<400> 8

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35 40 45

Phe Gln Lys Thr Gly Ser Phe Lys Ile Arg Gly Ala Leu Asn Ala Ile
50 55 60

Arg Gly Leu Ile Pro Asp Thr Pro Glu Glu Lys Pro Lys Ala Val Val
65 70 75 80

Thr His Ser Ser Gly Asn His Gly Gln Ala Leu Thr Tyr Ala Ala Lys
85 90 95

Leu Glu Gly Ile Pro Ala Tyr Ile Val Val Pro Gln Thr Ala Pro Asn
100 105 110

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Cys Lys Lys Leu Ala Ile Gln Ala Tyr Gly Ala Ser Ile Val Tyr Cys
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Asp Pro Ser Asp Glu Ser Arg Glu Lys Val Thr Gln Arg Ile Met Gln
    130                 135                 140

Glu Thr Glu Gly Ile Leu Val His Pro Asn Gln Glu Pro Ala Val Ile
145                 150                 155                 160

Ala Gly Gln Gly Thr Ile Ala Leu Glu Val Leu Asn Gln Val Pro Leu
                165                 170                 175

Val Asp Ala Leu Val Val Pro Val Gly Gly Gly Gly Met Val Ala Gly
            180                 185                 190

Ile Ala Ile Thr Ile Lys Ala Leu Lys Pro Ser Val Lys Val Tyr Ala
        195                 200                 205

Ala Glu Pro Ser Asn Ala Asp Asp Cys Tyr Gln Ser Lys Leu Lys Gly
    210                 215                 220

Glu Leu Thr Pro Asn Leu His Pro Pro Glu Thr Ile Ala Asp Gly Val
225                 230                 235                 240

Lys Ser Ser Ile Gly Leu Asn Thr Trp Pro Ile Ile Arg Asp Leu Val
                245                 250                 255

Asp Asp Val Phe Thr Val Thr Glu Asp Glu Ile Lys Tyr Ala Thr Gln
            260                 265                 270

Leu Val Trp Gly Arg Met Lys Leu Leu Ile Glu Pro Thr Ala Gly Val
        275                 280                 285

Ala Leu Ala Ala Val Leu Ser Gln His Phe Gln Thr Val Ser Pro Glu
    290                 295                 300

Val Lys Asn Val Cys Ile Val Leu Ser Gly Gly Asn Val Asp Leu Thr
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Ser Leu Asn Trp Val Gly Gln Ala Glu Arg Pro Ala Pro Tyr Gln Thr
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Val Ser Val
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<210> 9
<211> 1023
<212> DNA
<213> Homo sapiens

<400> 9

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aatcttttct tcaaatgtga actcttccag aaaacaggat cttttaagat tcgtggtgct   180
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ctcaatgccg tcagaagctt ggttcctgat gctttagaaa ggaagccgaa agctgttgtt   240
actcacagca gtggaaacca tggccaggct ctcacctatg ctgccaaatt ggaaggaatt   300
cctgcttata ttgtggtgcc ccagacagct ccagactgta aaaaacttgc aatacaagcc   360
tacggagcgt caattgtata ctgtgaacct agtgatgagt ccagagaaaa tgttgcaaaa   420
agagttacag aagaaacaga aggcatcatg gtacatccca accaggagcc tgcagtgata   480
gctggacaag ggacaattgc cctggaagtg ctgaaccagg ttcctttggt ggatgcactg   540
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aaacctagtg tgaaggtata tgctgctgaa ccctcaaatg cagatgactg ctaccagtcc   660
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ctcattgaac ctacagctgg tgttggagtg gctgctgtgc tgtctcaaca ttttcaaact   900
gtttccccag aagtaaagaa catttgtatt gtgctcagtg gtggaaatgt agacttaacc   960
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<210> 10
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<212> PRT
<213> Homo sapiens

<400> 10

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Ile Leu Asn Gln Leu Thr Gly Arg Asn Leu Phe Phe Lys Cys Glu Leu
        35                  40                  45

Phe Gln Lys Thr Gly Ser Phe Lys Ile Arg Gly Ala Leu Asn Ala Val
    50                  55                  60

Arg Ser Leu Val Pro Asp Ala Leu Glu Arg Lys Pro Lys Ala Val Val
65                  70                  75                  80

Thr His Ser Ser Gly Asn His Gly Gln Ala Leu Thr Tyr Ala Ala Lys
                85                  90                  95

Leu Glu Gly Ile Pro Ala Tyr Ile Val Val Pro Gln Thr Ala Pro Asp
            100                 105                 110

Cys Lys Lys Leu Ala Ile Gln Ala Tyr Gly Ala Ser Ile Val Tyr Cys
        115                 120                 125

Glu Pro Ser Asp Glu Ser Arg Glu Asn Val Ala Lys Arg Val Thr Glu
    130                 135                 140

Glu Thr Glu Gly Ile Met Val His Pro Asn Gln Glu Pro Ala Val Ile
145                 150                 155                 160

Ala Gly Gln Gly Thr Ile Ala Leu Glu Val Leu Asn Gln Val Pro Leu
                165                 170                 175
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Val Asp Ala Leu Val Val Pro Val Gly Gly Gly Gly Met Leu Ala Gly
            180                 185                 190

Ile Ala Ile Thr Val Lys Ala Leu Lys Pro Ser Val Lys Val Tyr Ala
        195                 200                 205

Ala Glu Pro Ser Asn Ala Asp Asp Cys Tyr Gln Ser Lys Leu Lys Gly
    210                 215                 220

Lys Leu Met Pro Asn Leu Tyr Pro Pro Glu Thr Ile Ala Asp Gly Val
225                 230                 235                 240

Lys Ser Ser Ile Gly Leu Asn Thr Trp Pro Ile Ile Arg Asp Leu Val
                245                 250                 255

Asp Asp Ile Phe Thr Val Thr Glu Asp Glu Ile Lys Cys Ala Thr Gln
            260                 265                 270

Leu Val Trp Glu Arg Met Lys Leu Leu Ile Glu Pro Thr Ala Gly Val
        275                 280                 285

Gly Val Ala Ala Val Leu Ser Gln His Phe Gln Thr Val Ser Pro Glu
    290                 295                 300

Val Lys Asn Ile Cys Ile Val Leu Ser Gly Gly Asn Val Asp Leu Thr
305                 310                 315                 320

Ser Ser Ile Thr Trp Val Lys Gln Ala Glu Arg Pro Ala Ser Tyr Gln
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Ser Val Ser Val
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<211> 1672
<212> DNA
<213> Mus musculus

<400> 11

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tgagaaggaa gccgccgtgc cagaggcagc agagaaccat gtgtgctcag tactgcatct    240
cctttgctga tgttgaaaaa gctcatatca acattcaaga ctctatccac ctcaccccag    300
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tcttccagaa aactgggtct tttaagattc gaggtgccct taatgccatc agaggcttaa    420
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gcatcttggt ccatcccaac caggagcctg cagtgatagc tggacaagga acaattgccc    720
tggaagtgct gaaccaggtt cccttggtag atgcactggt ggtaccagta ggaggaggag    780
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ctgctgagcc ctcgaatgca gatgactgct accagtctaa actgaaagga gaactgaccc    900
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